



GP1645
Jhu

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

<i>In re</i> Application of)	
)	Group Art Unit: 1645
ZHELNIN and BLOOMQUIST)	
)	Examiner: S. Gucker
Serial No. 09/899,532)	
)	
Filing Date: July 6, 2001)	Docket No. 02973.00040

For: **HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR**

SUBMISSION OF SUBSTITUTE DECLARATION UNDER 37 C.F.R. § 1.131

U.S. Patent and Trademark Office
220 20th Street S.
Customer Window, Mail Stop Amendment
Crystal Plaza Two, Lobby, Room 1B03
Arlington, VA 22202

Dear Sir:

Applicants responded on June 25, 2004 to the Office Action mailed February 25, 2004 in the application referenced above. The response included a declaration of the inventors under 37 C.F.R. § 1.131, which included Exhibits 1-10. The declaration stated that the dates on Exhibits 1-10 had been redacted; however, the Exhibits 1-10 filed together with the declaration inadvertently contained dates.

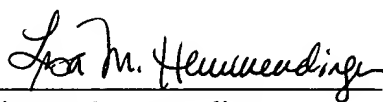
A substitute declaration with Exhibits 1-10 accompanies this paper. The declaration itself is a copy of the one filed June 25, 2004. Exhibits 1-10 are identical to those filed June 25, 2004 except that the dates have been redacted.

Please substitute the declaration and exhibits that accompany this paper for those filed June 25, 2004. Please discard the declaration and exhibits filed June 25, 2004 and delete all copies of the declaration and exhibits that may have been scanned electronically.

We believe no fee is associated with this request. If a fee is required, please charge our Deposit Account No. 19-0733.

Respectfully submitted,
BANNER & WITCOFF, LTD.

Date: July 6, 2004

By: 
Lisa M. Hemmendinger
Registration No. 42,653

Customer No. 22907



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)
ZHELNIN and BLOOMQUIST) Group Art Unit: 1645
Serial No. 09/899,532) Examiner: S. Gucker
Filing Date: July 6, 2001) Docket No. 02973.00040

For: HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR

DECLARATION UNDER 37 C.F.R. § 1.131

U.S. Patent and Trademark Office
220 20th Street S.
Customer Window, Mail Stop Non-Fee Amendment
Crystal Plaza Two, Lobby, Room 1B03
Arlington, VA 22202

Dear Sir:

We, Leonid Zhelnin and Brian Bloomquist, declare as follows:

1. We are the named inventors of the subject matter claimed in the application referenced above.
2. Prior to March 2, 2000, we reduced to practice the subject matter of claims 1-8 and 12 of the application referenced above. The dates on the attached exhibits have been redacted; however, all the work described in this declaration was performed in the United States prior to March 2, 2000.
3. Prior to March 2, 2000, we monitored search results from a program (Gene Agent) that automatically checked sequences released into the public domain for homology to the orexin and NPY1 receptors. Prior to March 2, 2000, we received reports from the orexin-

and NPY1-receptor Gene Agent searches, respectively, indicating that DNAs with accession numbers EM:AC005961 (Homo sapiens Chromosome 11q12.2 PAC pDJ32L16 genomic DNA) and GB:g3823006 (Human sperm genomic library) both had homology to the orexin and NPY1 receptor sequences. Copies of the reports are attached as Exhibit 1. Sequence analysis revealed these DNAs to be overlapping and that AC00596 contained 154,647 nucleotides comprising what appeared to be at least five exons with homology to the orexin receptor. A copy of BLAST comparisons of the translated five exons with the amino acid sequence of the orexin receptor is attached as Exhibit 2.

4. Prior to March 2, 2000, we used sequence information from AC005961 to amplify by polymerase chain reaction (PCR) amplification two PCR products of 234 and 111 bp from genomic DNA. The longer 234 bp clone included both transmembrane domains (TM 1 and 2) of the putative GPCR. A copy of the nucleotide sequence of the PCR product is attached as Exhibit 3.

5. We designed primers to the 5'- and 3'-regions of the 234 bp clone, and 5'- and 3'-RACE amplifications were carried out to clone the full coding region of the putative GPCR. The reverse primers used in the strategy were termed "6A1-85B" and "6A1-126B" and are shown on pages 2 and 3 of Leonid Zhelnin's laboratory notebook no. RB53651. Copies are provided as Exhibit 4.

6. Prior to March 2, 2000, we obtained two 5'-RACE clones (~220 and ~320 bp) from human heart cDNA; sequence analysis of the 5'-RACE clone 5GA1 revealed that it encodes a peptide with homology to the N-terminal 105 amino acids of NPY1. A copy of page 47 of Leonid Zhelnin's laboratory notebook no. RB53651 showing a ClustalW-formatted alignment of the amino acid sequence encoded by 5GA1 and the amino acid sequence of the neuropeptide Y-1

receptor (NPY-1R.pap) is provided as Exhibit 5. The position of the putative START methionine codon (ATG) in clone 5GA1 was consistent with clone 5GA1 being similar to the NPY-1 and orexin-2 receptors. The identity of this ATG as the true START codon was unconfirmed, however, because the open reading frame (ORF) was not closed upstream of the 5'-most ATG.

7. Sequence analysis of the 3'-RACE amplicon (~0.9 kb in length; 3'-RACE #2 clone) revealed that this clone contained sequences homologous to a GPCR through TM6. The primers used in the 3'-RACE strategy were termed "6A1-F32" and "6A1-F41" and are shown on pages 4 and 5 of Leonid Zhelnin's laboratory notebook no. RB53651. Copies are provided as Exhibit 6. However, the 3'-RACE amplicon lacked both a TM7 domain and corresponding STOP codon. A complete clone was electronically assembled from the 3'-RACE amplicon and clone 5GA1 to create a 1047-bp sequence contig, which encoded 349 amino acids and which was named GA1. A copy of page 53 of Leonid Zhelnin's laboratory notebook no. RB53651 showing the electronically assembled sequence is provided as Exhibit 7.

8. Prior to March 2, 2000, GA1 was used as template to search the Image Consortium database for novel expressed sequence tags (ESTs, which are cDNAs) with identity to GA1 to identify the missing 3'-end. Three Image clones from human kidney were identified and found to have similarity based on our previous sequence analysis. Identification of the three Image clones was recorded on page 61 of Leonid Zhelnin's laboratory notebook no. RB53651; a copy is provided as Exhibit 8.

9. Sequence analysis of Image clone 2055185 confirmed the putative START methionine because sequence analysis revealed it to contain an in-frame STOP codon upstream

of the putative START methionine. This sequence information is summarized on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651; a copy is provided as Exhibit 9.

10. Under our direction the 3'-ends of the Image cDNAs (from the NCI_CGAP_Kid12 and Soares NFL_T_GBC_S1 libraries) were sequenced. One of the Image clones had an extended 3'-end that included the presence of a 710-bp intron followed by what appeared to be further exonic sequence.

11. The sequence immediately downstream of the intron of this Image cDNA clone was used as the query to search (via the BLAST algorithm) the genomic sequence within AC005961 to identify the missing 3'-coding region. Prior to March 2, 2000, BLAST analysis identified the missing 271 nucleotides of the 3'-end of the coding region of the GPCR. This sequence information is summarized on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. See Exhibit 9.

12. Prior to March 2, 2000, we amplified clones containing the complete 1293-bp ORF from both human heart and brain cDNA by PCR (using Marathon-Ready cDNA libraries, Clontech) and recorded this information on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. See Exhibit 9.

13. Also prior to March 2, 2000, the coding sequence of the full-length cDNA clone was confirmed by sequence analysis of a full-length amplicon generated by PCR from human brain cDNA. This sequence was recorded on pages 95-97 of Leonid Zhelnin's laboratory notebook no. RB53651; copies of these pages are provided as Exhibit 10. The coding sequence is contained within SEQ ID NO:1 of our provisional application Serial No. 60/215,523 and within SEQ ID NO:1 of our utility application 09/899,532. This coding sequence encodes the 431 amino acid sequence shown in SEQ ID NO:2 of both the provisional and utility applications.

14. All statements made herein of our own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: June 25, 2004

Brian T. Bloomquist
Brian Bloomquist, Ph.D.

Dated: June 25, 2004

Leonid Zhelnin
Leonid Zhelnin, Ph.D.

Home Menu	Projects	Diary	Sex Analysis	Utilities	Login / Logout	Help
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```
Project ID: oraxin      Project Name: oraxin receptor homology search
Created:      Created By: Zhelain, Leonid
Modified:     Modified By: lt_account, Admin
Status:       Current User: Zhelain, Leonid (WRITE)
Today's Date: Num Sigs:   7
```

Analysts' Date: _____

These results are saved. Use the buttons to change the state of these results.

Save These Results **Delete These Results**

Maximum Number of Hits per Hit Class

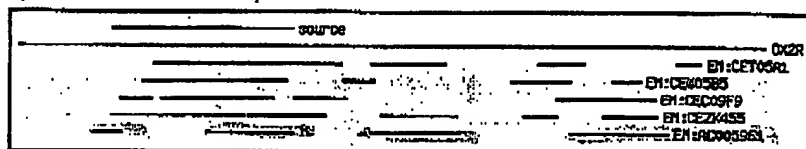
Trans. Protein: 5

Feature roll-up: C Off & On

Redisplay

View parameters

Protein Agent



☐ orexin:OX2R:1

Hit ID	P-Value	Ident.	Description				Hit Class
<input checked="" type="checkbox"/> EM:CM05A1:5 Result Details	2.5e-17	40	Caenorhabditis elegans cosmid T05A1				Trans. Protein
	Feature Source	Description				Feature Metric	Value
		Left End	Right End	Strand	Component Description	Component Metric	Value
		81	134	+			
Hit ID	P-Value	Ident.	Description				Hit Class
<input checked="" type="checkbox"/> EM:CM05B5:5 Result Details	4.7e-17	33	Caenorhabditis elegans cosmid W05B5				Trans. Protein
	Feature Source	Description				Feature Metric	Value
		Left End	Right End	Strand	Component Description	Component Metric	Value
		74	133	+			
Hit ID	P-Value	Ident.	Description				Hit Class
<input checked="" type="checkbox"/>	7.4e-17	35	Caenorhabditis elegans cosmid C09F9				Trans. Protein

EM:CEC0979.5 Result Details	source					Component Metric	Value
		Left End	Right End	Strand	Component Description		
		85	132	+			
Hit ID	P-value	% ident.	Description				Hit Class
EM:CEK455.5 Result Details	8.3e-14	26	Caenorhabditis elegans cosmid 2K455				Trans. Protein
	Feature source	Description				Feature Metric	Value
		Left End	Right End	Strand	Component Description		
		56	134	+			
Hit ID	P-value	% ident.	Description				Hit Class
EM:ACD03961.1 Result Details	1.8e-12	32	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.				Trans. Protein
	Feature source	Description				Feature Metric	Value
		Left End	Right End	Strand	Component Description		
		112	163	+			

Requested by: Zhelmin, Leonid on

Main Menu Project Query Seq Analysis Utilities Login/Logout Help

Project ID: orexin Project Name: orexin receptor homology search
 Created: Created By: Zhelmin, Leonid
 Modified: Modified By: It Account, Admin
 Status: Current User: Zhelmin, Leonid (WRITER)
 Today's Date: Num Seqs: 7

Project Members

Project Status

Analysis Tools

Create Agent

Sequences (7 of 7 shown, 7 Active):

Sequence ID	Type	Parent	Created By	Created	Status
<u>orexin:q3823006:1</u>	DNA	GB:q3823006	Zhelmin, L.		OPEN
HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.					
<u>orexin:AC005961:1</u>	DNA	EM:AC005961	Zhelmin, L.		OPEN
*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.					
<u>orexin:framel AC005961:1</u>	PRT		Zhelmin, L.		OPEN
<u>orexin:neworex1.pep:1</u>	PRT		Zhelmin, L.		OPEN
<u>orexin:G2897124:1</u>	PRT	ST:G2897124	Zhelmin, L.		OPEN
OREXIN RECEPTOR-1.					
<u>orexin:OX2R:1</u>	PRT		Zhelmin, L.		OPEN
P1:G2897128 - orexin receptor-2 - Homo sapiens (human)					
<u>orexin:AF041243:1</u>	RNA	EM:AF041243	Zhelmin, L.		OPEN
Homo sapiens orexin receptor-1 mRNA, complete cds.					

Manage Sequences

Add Sequences

Gene Agent Results (10 of 166 shown, 166 active):

Agent Name	Results	Started On	Description	Status	Method	Job Status
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed

List All Gene Agent Results

No Project Annotation

List All Annotations

View All Project Annotations

Add New Annotations

Requested by: Zhelmin, Leonid

LifeTools
biology in silico**Query Detail**[Main Menu](#)[Projects](#)[Query](#)[Seq Analysis](#)[Utilities](#)[Login / Logout](#)[Help](#)Sequence: orexin:AC005961:1 [Add Sequence Annotation](#)

Entries with the same Physical Sequence EM:AC005961 GB:g3859648 Image1ga:g3859648:1 Newgag:AC005961:1		FASTA
General Information About The Entry		
Sequence ID	AC005961	
Version	1	
Sequence Description	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase unordered pieces. , 8	
Project	orexin	
Project Name	orexin receptor homology search	
Molecule	DNA	
Sequence Information		
Length	154647	

 **INCYTE PHARMACEUTICALS, INC.**

Sequences producing High-scoring Segment Pairs:

Reading	High	Small Su	Proba
Frame	Score		P(N)

AC005961 *** SEQUENCING IN PROGRESS *** Homo sapien.. +2 103 1.8e-

Score = 103 (48.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12
Identities = 17/52 (32%), Positives = 33/52 (63%), Frame = (+2)

Query: 112 LVVDITETWFFGQSLCKVIPYLQTVSVSVLTLSCIALDRWYAICHPLMFK 163
L+ D++ G +CK++P++Q+ +V +LT++CIA++R + HP K
Sbjct: 48452 LMYDLSYFLTAGAFICKKVPFVQSTAVVTEILIMTCIAVERHQGLVHPFKMK 48607

Score = 88 (41.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12
Identities = 15/54 (27%), Positives = 31/54 (57%), Frame = (+3)

Query: 210 CDERWGGEIYPKMYHICFFLVTYMAPLCMLVLAQLQIFRKLWCRQIPGTSSVVQ 263
C E W ++ K+Y ++ ++ PL +M++ Y +I +LW ++ G SV++
Sbjct: 56082 CLBEWTSPPVHQKIYTTFFILVILFLLPLMVMLILYSKIGYELWIKRVRGDSVLR 56243

Score = 71 (33.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12
Identities = 15/54 (27%), Positives = 26/54 (48%), Frame = (+1)

Query: 329 VFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSGKFRESFKAAPSCC 382
+ G F D T+ F + ++NS NPI+Y F++ F++ +A C
Sbjct: 59380 ISGNFEKEYDDVTIKMIFAIVQIIGFSNSICNPVYAFMNENFKKNVLSAVCYC 59541

Score = 47 (22.1 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12
Identities = 9/17 (52%), Positives = 11/17 (64%), Frame = (+2)

Query: 46 EYLHPKEYEWVLIAGYI 62
EY H +E W LI+ YI
Sbjct: 29786 EYPHAEENWTLISQYI 29836

Score = 46 (21.6 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12
Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = (+3)

Query: 381 CCCLGVHH 388
CCCLG+ H
Sbjct: 148295 CCCLGLEH 148319

**Retrieve
FASTA Sequences**[Main Menu](#)[Projects](#)[Query](#)[Seq. Reports](#)[Utilities](#)[Login / Logout](#)[Help](#)Project ID: Newpage

Created:

Modified:

Status: **OPEN**

Today's Date:

Project Name: **Cloning new gene agent search sequences**Created By: **Zhelnin, Leonid**Modified By: **Zhelnin, Leonid**Current User: **Zhelnin, Leonid (WRITE)**Num Seqs: **30**

>Newpage:GA2:1 pcr product of ac ac1 primers of AC00596 genomic chromosome se
GTATGATTATCCTATTTTCCTTACTGCAGGTGCTTTCATTGCAAGATGGTGCCATTTGTCAGTCTACCGCTGTTGTGA
CAGAAATCCTCACTATGACCTGCATTGCTGTGGAAAGGCACCAGGGACTTGTGCATCCTTTAAATGAAGTGGCAATAC
ACCAACCGAAGGGCTTTCACAATGCTAGGTGAGGCCACTGGATGTGCCAATGGCAGTGTGAATGACATTCTTCA

Requested by: Zhelnin, Leonid on

 **INCYTE PHARMACEUTICALS, INC.**

6A1-5 RACE product

17. התאחדות העובדים ... התאחדות העובדים ...

1

2

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4

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P# 10

11

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20:

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32

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34

DATE _____

DAT

BAYER CORPORATION

SUBJECT

3' RACE

1

2

3

Translated Sequence

4

5

Range: 1 to 161

6

7

10 20 30 40 50
 AGTGACTCATCGCCCTGGCGCTTTTGGCAATGCTCTGGTGTCTACG
 TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCACAAGATGCA
 S V L I A L A L F G N A L V F Y V

8

9

TRANSLATION OF GA1.TXT [A]

10

11

60 70 80 90 100
 CCACTGGCGCTCGTCCGGTACGGTGGCAGTGOTTGTAGAAATAGACGA
 V T R S K A M R T V T N I F I C

12

13

TRANSLATION OF GA1.TXT [A]

14

15

110 120 130 140 150
 CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCATTCCCGTCACC
 GGAACCGCGACTCACTGGACGAGTAGTGGAAGAAGACGTAAGGGCAGTGG
 S L A L S D L L T F F C I P V T

16

17

TRANSLATION OF GA1.TXT [A]

18

19

150
 ATGAAGCCGAA
 TACTTCGGCTT
 M K P X

20

21

22

23

24

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26

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34

SIGNED BY

WITNESSED AND UNDERSTOOD BY

CROSS REFERENCES:

DATE

DATE

6A1 F41

New

Page 1

Noted 6A1

Noted 6A1

6A F32

to order
for labeling

3' race

41 22 100 167 53.9 70.0 3.5 56.7 60.4 56.8 48.1 48.1 -3.6 -8.3

CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCATTCCCGTCACC 27 -43.6 -109.5 -515.1
 CCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCATTCCCGTCACC 27 -43.0 -205.0 -536.4

32 74 100 115 52.2 75.4 1.7 54.9 50.6 56.0 48.0 48.1 -4.4 -8.3

GACCTGACCTACCTTCTTCTGCATTCCCGTCACC 25 -40.2 -102.9 -471.0

BAYER CORPORATION

Touch down PCR for GAT RACE

15	5 μ l cDNA template (Heart) (Brain)	1
108	36 μ l H ₂ O	2
15	5 μ l 10 \times cDNA Buffer	3
3	1 μ l dNTP Mix (10 mM)	4
3	1 μ l Ado cDNA polymerase mix (50 \times)	5
	43 μ l Final + 3 μ l AP1	6

Program 1 (preferred: use if GSP T_m > 70°C):PE DNA T_m = 100°CPE GeneAmp Systems 2400/9600
(or hot-lid thermal cycler):

• 94°C for 30 sec

• 5 cycles:

94°C 5 sec

72°C 4 min⁰

• 5 cycles:

94°C 5 sec

70°C 4 min⁰

• 20-25 cycles:

94°C 5 sec

68°C 4 min⁰

Heart	1	B126
	2	F32
	3	F41
Brain	4	B126
	5	F32
	6	F41

PRODUCT: Human Heart
Marathon-Ready™ cDNA

CATALOG #: 7404-1

LOT#: 9010719

STORAGE BUFFER:

- 10 mM Tricine-KOH (pH 9.2)
- 1 mM EDTA

STORAGE CONDITIONS:

- -20°C
- Avoid multiple freeze/thaw cycles.

SHELF LIFE:

1 year from date of receipt under
proper storage conditions

DESCRIPTION:

Marathon-Ready cDNA is high-quality, double-stranded cDNA which has been ligated to the Marathon™ Adaptor and is ready for use as a template in 5' and 3' Marathon RACE reactions. In many cases, the full-length cDNA can then be obtained by end-to-end amplification or standard cloning. Enough material is provided for 30 50- μ l Marathon RACE reactions.

CONCENTRATION: \approx 0.1 ng/ μ lPOLY A⁺ RNA SOURCE:

Normal, whole hearts pooled from 3 male Caucasians, ages 28-47; cause of death: trauma

No further RNA source information is available.

SIGNED BY

DATE

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DATE

CROSS REFERENCES

BAYER CORPORATION

61

SUBJECT

mage clones matching 6A1

Im	2055532	g4001837	1
Im	2055185	g4002759	2
Im	2091776	g9187861	3
			4
			5
			6
			7

DNA vs EST Homology Search

source	g4001837
GB:g400 337	
GB:g400 759	
GB:g4187861	

g4001837

Hit ID #	P-Value	% ident.	Description
GB:g4001837 (Detail)	0	100	tb27a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

Analysis Results: 28499

http://lifetools-a.wh.bayer.com/cgi-bin/incyte/LifeTools/2.0/LT_viewer?id=28499

GB:g4002759 (Detail)	0	100	tb23d09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

AM

GB:g4187861 (Detail)	6.2e-43	100	tc67e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens
Feature	Start	Stop	Description
source	3	127	

Acc. Num.	Image/Unigene TIGR Indices	Insert Length	Read Length	HQSS	Source (Age/Sex)	
AI307658	Im:2055532 Hs.181638	1414	432	419	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))	20 27 28 29
AI308124	Im:2055185 Hs.181638	1308	432	429	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))	30 31 32
AI378908	Im:2091776 Hs.181638	404	364		Soares_NFL_T_GBC_S1 library made from pooled	33 34

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCE

NRX-like clow and primors.

$$\neq 10, 14, 15, 1$$

DNA sequence 1902 b.p. TGGGCTCGAGG ... CTGATTCCTC 11 bases

	1
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SIL	3
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	6
	7
	8
	9
	10
↓ C AA 66	11
STY	12
C ST 66	13
6 S AAQC	14
	15
C L 6A	16
6 S AAQC	17
	18
TA	19
	20
	21
	22
	23
	24
	25
	26
	27
	28
	29
	30
	31
	32
	33
	34

DATE _____

DATE _____

CROSS REFERENCES:

95

BAYER CORPORATION

SUBJECT

Sequencing results of LG21/PT7Blue

1. Check if I. Taylor going to clone P.E. receptor and when?

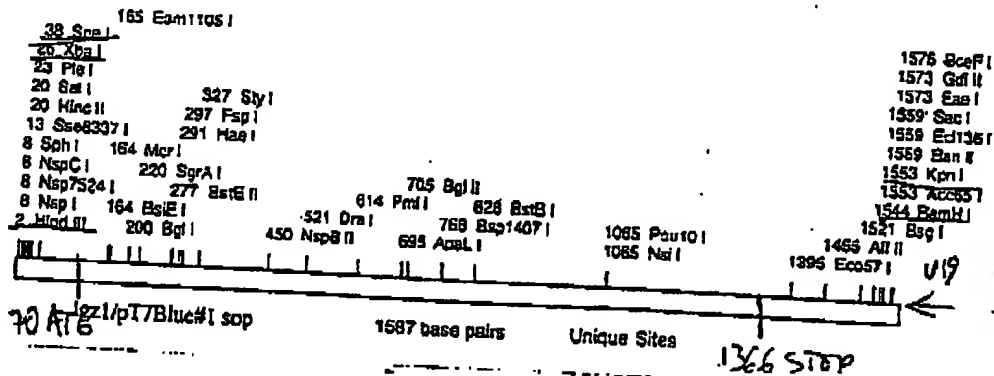
1. Clone #1 sop is ok with one polymorphic

DNA Strider™ 1.2

lg21/PT7Blue#1 sop -> Graphic Map

DNA sequence 1587 b.p. ccagccgacgacg ... ccgcgcgtttacc linear

432 AA



2) Clone #7 K. Brain is good (same orientation) with ttt -> ttc (Phe) 917 AA

3) clone #16 K. Hart is good with atc -> att (Ile) 216 AA

↓ cloned using TA-kt in penta 310 fls.

Xba/Bam 3.1(-)
Kpn(L)

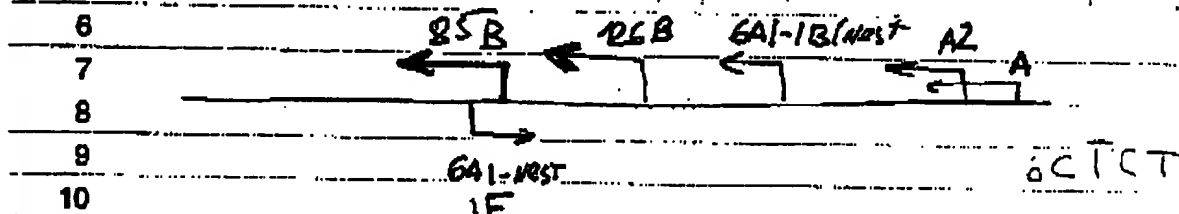
SIGNED BY

BAYER CORPORATION

SUBJECT

5' RACE 641

1	9	1	85	85	54.1	74.1	4.9	54.1	56.8	61.7	48.2	60.0	-3.3	-7.0		
2			CGCTCTAATACGACTGCTATAGGC 27 -43.0 -205.0 -536.4												GGTCATACGCTAGACATAGAC 25 -41.9 -184.5 -470.9	6A-8
3																
4	10	1	126	126	54.8	77.0	1.7	56.0	56.8	59.6	48.2	49.0	-3.3	-7.8		
			CGCTCTAATACGACTGCTATAGGC 27 -43.0 -205.0 -536.4												GGTCATACGCTAGACATAGAC 25 -40.2 -182.9 -471.0	6A1-



GA1.txt Translated Sequence

Sequence Range: 1 to 161

Range: 1 to 161
Double strand probe

6A1-25B 6A1-FY
→

10 20 30 40 50
 CACCTCTGTG ACCAG AGTGTACTCATGCGCCCTGGCCCTCTTTGGCAATGCTGCTGGTGTCTACGT
 TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCCACAAGATGCA
 S V L I A L A L F G N A L V E Y V

pro

TRANSLATION OF GA1.TXT [A]

641-126B

60 70 80 90 100
GGTGACCCGCGAGCAAGGCCATGCGGCACCGTCACCAACATCTTTATCTGCT
CCACTGGCGCTCGTTCGGGTACGGGTGGCAGTCGTTGTAGAANTAGACGA
V T R S K A M R T V T N I F I C>

TRANSLATION OF GAL.TXT [A]

← GA1-1B GA2-BA2 GA1-BA1 (long)
110 120 130 140 150
CCTTGGCGCTCAGTGACCTGCTATCACCTCTCTTCGATTCCCGTCACC
CGAACCGCGACTCTCTGACGASTAGTGGAGAGTACGCTATGCGCAGTGG
S L A H S U E F C I P V T>
TRANSLATION OF GA1.TXT [A]

160

ATGAAGCCGAA

~~SECRET~~CGGCTT

14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1

5 primers for 5' RACE

probe:

SIGNED BY

WITNESSED AND UNDERSTOOD BY

DATE _____

CROSS REFERENCES:

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